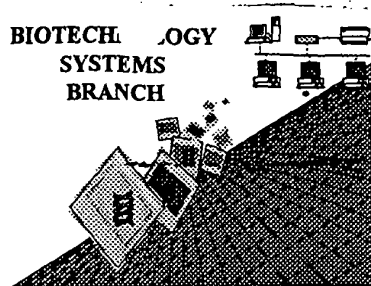


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



OCT 25 2000

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/303,518A  
Source: 1631  
Date Processed by STIC: 10/12/2000

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

## Raw Sequence Listing Error Summary

OCT 25 2000

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/308/5784600/2900

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2      Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3      Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4      Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5      Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6      Variable Length      Sequence(s)      contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7      PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)                     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8      Skipped Sequences (OLD RULES)      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9      Skipped Sequences (NEW RULES)      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10      Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11      Use of <213>Organism (NEW RULES)      Sequence(s)              are missing this mandatory field or its response.
- 12      Use of <220>Feature (NEW RULES)      Sequence(s)      are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13      PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

#72

10-27-00  
P2.

1631

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/303,518A

DATE: 10/12/2000  
 TIME: 15:29:08

Input Set : N:\jumbos\09303518  
 Output Set: N:\CRF3\10122000\I303518A.raw

Does Not Comply  
 Corrected Diskette Needed

P.6

3 <110> APPLICANT: Scarlato, Enzo  
 4 Masignani, Vega  
 5 Rappuoli, Rino  
 6 Pizza, Mariagrazia  
 7 Grandi, Guido  
 9 <120> TITLE OF INVENTION: Neisserial Antigens  
 11 <130> FILE REFERENCE: CHIR0160  
 13 <140> CURRENT APPLICATION NUMBER: 09/303,518A  
 14 <141> CURRENT FILING DATE: 1999-04-30  
 16 <150> PRIOR APPLICATION NUMBER: PCT/IB98/01665  
 17 <151> PRIOR FILING DATE: 1998-10-09  
 19 <160> NUMBER OF SEQ ID NOS: 1098  
 21 <170> SOFTWARE: PatentIn Ver. 2.1  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 506  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Neisseria meningitidis  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: unsure  
 30 <222> LOCATION: (18)  
 31 <223> OTHER INFORMATION: N=Unknown  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: unsure  
 35 <222> LOCATION: (67)  
 36 <223> OTHER INFORMATION: N=Unknown  
 38 <220> FEATURE:  
 39 <221> NAME/KEY: unsure  
 40 <222> LOCATION: (102)  
 41 <223> OTHER INFORMATION: N=Unknown  
 43 <220> FEATURE:  
 44 <221> NAME/KEY: unsure  
 45 <222> LOCATION: (154)  
 46 <223> OTHER INFORMATION: N=Unknown  
 48 <220> FEATURE:  
 49 <221> NAME/KEY: unsure  
 50 <222> LOCATION: (276)  
 51 <223> OTHER INFORMATION: N=Unknown  
 53 <220> FEATURE:  
 54 <221> NAME/KEY: unsure  
 55 <222> LOCATION: (487)  
 56 <223> OTHER INFORMATION: N=Unknown  
 58 <400> SEQUENCE: 1  
 W-> 59 atgaaacaga cagtcaanat gcttgccgcc gccctgattg ccttgggctt gaaccgaccg 60  
 W-> 60 gtgtggncgg atgacgtatc ggattttcgg gaaaacttgc ancgggcagc acagggaaat 120  
 W-> 61 gcagcagccc aatacaattt gggcgcaatg tatntacaaa ggacgcgcgt gcgcccggat 180  
 W-> 62 gatgctgaag cggtcagatg gtatcggcag ccggcggaac aggggttagc ccaagcccaa 240  
 W-> 63 tacaatttgg gctggatgta tgccaacggg cgcgcngtgc gccaaagatga taccgaagcg 300

## RAW SEQUENCE LISTING

DATE: 10/12/2000

PATENT APPLICATION: US/09/303,518A

TIME: 15:29:08

Input Set : N:\jumbos\09303518

Output Set: N:\CRF3\10122000\I303518A.raw

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64 gtcagatggt atcggcaggc ggcagcgag ggggttggtcc aagcccaata caattgggc 360
65 gtgatatatg ccgaaggacg tggagtgcgc caagacgatg tcgaagcgtt cagatgggtt 420
66 cggcaggcgg cagcgagggg ggtagcccaa gcccaaaaca atttggcgt gatgtatgcc 480
W--> 67 gaaagancgc gcgtgcgcca agaccg 506
70 <210> SEQ ID NO: 2
71 <211> LENGTH: 168
72 <212> TYPE: PRT
73 <213> ORGANISM: Neisseria meningitidis
75 <220> FEATURE:
76 <221> NAME/KEY: UNSURE
77 <222> LOCATION: (6)
78 <223> OTHER INFORMATION: X= any amino acid
80 <220> FEATURE:
81 <221> NAME/KEY: UNSURE
82 <222> LOCATION: (23)
83 <223> OTHER INFORMATION: X= any amino acid
85 <220> FEATURE:
86 <221> NAME/KEY: UNSURE
87 <222> LOCATION: (34)
88 <223> OTHER INFORMATION: X= any amino acid
90 <220> FEATURE:
91 <221> NAME/KEY: UNSURE
92 <222> LOCATION: (52)
93 <223> OTHER INFORMATION: X= any amino acid
95 <220> FEATURE:
96 <221> NAME/KEY: UNSURE
97 <222> LOCATION: (92)
98 <223> OTHER INFORMATION: X= any amino acid
100 <220> FEATURE:
101 <221> NAME/KEY: UNSURE
102 <222> LOCATION: (163)
103 <223> OTHER INFORMATION: X = any amino acid
105 <400> SEQUENCE: 2
W--> 106 Met Lys Gln Thr Val Xaa Met Leu Ala Ala Ala Leu Ile Ala Leu Gly
107 1 5 10 15
W--> 109 Leu Asn Arg Pro Val Trp Xaa Asp Asp Val Ser Asp Phe Arg Glu Asn
110 20 25 30
W--> 112 Leu Xaa Ala Ala Ala Gln Gly Asn Ala Ala Ala Gln Tyr Asn Leu Gly
113 35 40 45
W--> 115 Ala Met Tyr Xaa Gln Arg Thr Arg Val Arg Arg Asp Asp Ala Glu Ala
116 50 55 60
118 Val Arg Trp Tyr Arg Gln Pro Ala Glu Gln Gly Leu Ala Gln Ala Gln
119 65 70 75 80
W--> 121 Tyr Asn Leu Gly Trp Met Tyr Ala Asn Gly Arg Xaa Val Arg Gln Asp
122 85 90 95
124 Asp Thr Glu Ala Val Arg Trp Tyr Arg Gln Ala Ala Ala Gln Gly Val
125 100 105 110
127 Val Gln Ala Gln Tyr Asn Leu Gly Val Ile Tyr Ala Glu Gly Arg Gly
128 115 120 125

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RAW SEQUENCE LISTING                      DATE: 10/12/2000  
 PATENT APPLICATION: US/09/303,518A        TIME: 15:29:08

Input Set : N:\jumbos\09303518  
 Output Set: N:\CRF3\10122000\I303518A.raw

```

130 Val Arg Gln Asp Asp Val Glu Ala Val Arg Trp Phe Arg Gln Ala Ala
131      130      135      140
133 Ala Gln Gly Val Ala Gln Ala Gln Asn Asn Leu Gly Val Met Tyr Ala
134 145      /      150      155      160
W--> 136 Glu Arg Xaa Arg Val Arg Gln Asp
137      165
140 <210> SEQ ID NO: 3
141 <211> LENGTH: 597
142 <212> TYPE: DNA
143 <213> ORGANISM: Neisseria meningitidis
145 <400> SEQUENCE: 3
146 atgaaacaga cagtcaaatg gcttgccgcc gccctgattg ccttgggctt gaaccgagcg 60
147 gtgtggggcg atgacgtatc ggattttcgg gaaaacttgc aggcggcagc acaggggaaat 120
148 gcagcagccc aatacaattt gggcgcaatg tattacaaag gacgcggcgt gcgcccggat 180
149 gatgctgaag cggtcagatg gtatcggcag gcggcggaac aggggttagc ccaagcccaa 240
150 tacaatttgg gctggatgta tgccaacggg cgcggcgtgc gccaatgata taccgaagcg 300
151 gtcagatggt atcggcaggg gcagcgcaag ggggttgc ccagccaata caatttgggc 360
152 gtgatatatg ccgaaggacg tggagtgcgc caagacgatg tcgaagcggg cagatggttt 420
153 cgcagggcgg cagcgagggg ggtagcccaa gcccaaaaca atttgggctg gatgtatgcc 480
154 gaaagacggc gcgtgcgcca agaccgcgcc cttgcacaag aatggtttgg caaggcttgt 540
155 caaaacggag accaagacgg ctgcgacaat gaccaacgcc tgaaggcggg ttattga 597
158 <210> SEQ ID NO: 4
159 <211> LENGTH: 198
160 <212> TYPE: PRT
161 <213> ORGANISM: Neisseria meningitidis
163 <400> SEQUENCE: 4
164 Met Lys Gln Thr Val Lys Trp Leu Ala Ala Ala Leu Ile Ala Leu Gly
165      1      5      10      15
167 Leu Asn Arg Ala Val Trp Ala Asp Asp Val Ser Asp Phe Arg Glu Asn
168      20      25      30
170 Leu Gln Ala Ala Gln Gly Asn Ala Ala Ala Gln Tyr Asn Leu Gly
171      35      40      45
173 Ala Met Tyr Tyr Lys Gly Arg Gly Val Arg Arg Asp Asp Ala Glu Ala
174      50      55      60
176 Val Arg Trp Tyr Arg Gln Ala Ala Glu Gln Gly Leu Ala Gln Ala Gln
177      65      70      75      80
179 Tyr Asn Leu Gly Trp Met Tyr Ala Asn Gly Arg Gly Val Arg Gln Asp
180      85      90      95
182 Asp Thr Glu Ala Val Arg Trp Tyr Arg Gln Ala Ala Ala Gln Gly Val
183      100      105      110
185 Val Gln Ala Gln Tyr Asn Leu Gly Val Ile Tyr Ala Glu Gly Arg Gly
186      115      120      125
188 Val Arg Gln Asp Asp Val Glu Ala Val Arg Trp Phe Arg Gln Ala Ala
189      130      135      140
191 Ala Gln Gly Val Ala Gln Ala Gln Asn Asn Leu Gly Val Met Tyr Ala
192 145      150      155      160
194 Glu Arg Arg Gly Val Arg Gln Asp Arg Ala Leu Ala Gln Glu Trp Phe
195      165      170      175
197 Gly Lys Ala Cys Gln Asn Gly Asp Gln Asp Gly Cys Asp Asn Asp Gln

```

RAW SEQUENCE LISTING                      DATE: 10/12/2000  
 PATENT APPLICATION: US/09/303,518A        TIME: 15:29:08

Input Set : N:\jumbos\09303518  
 Output Set: N:\CRF3\10122000\I303518A.raw

```

198                               180           185           190
200 Arg Leu Lys Ala Gly Tyr
201                               195
204 <210> SEQ ID NO: 5
205 <211> LENGTH: 273
206 <212> TYPE: DNA
207 <213> ORGANISM: Neisseria meningitidis
209 <400> SEQUENCE: 5
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211 gtgtgggcgg atgacgtatc ggattttcgg gaaaacttgc aggcggcagc acagggaaat 120
212 gcagcagccc aaaacaattt gggcgtgatg tatgccgaaa gacgcggcgt gcgccaagac 180
213 cgcgcccttg cacaagaatg gcttggcaag gcttgtcaaa acggatacca agacagctgc 240
214 gacaatgacc aacgcctgaa agcgggttat tga                               273
217 <210> SEQ ID NO: 6
218 <211> LENGTH: 90
219 <212> TYPE: PRT
220 <213> ORGANISM: Neisseria meningitidis
222 <400> SEQUENCE: 6
223 Met Lys Gln Thr Val Lys Trp Leu Ala Ala Leu Ile Ala Leu Gly
224 1                               5           10           15
226 Leu Asn Gln Ala Val Trp Ala Asp Asp Val Ser Asp Phe Arg Glu Asn
227                               20           25           30
229 Leu Gln Ala Ala Gln Gly Asn Ala Ala Ala Gln Asn Asn Leu Gly
230 35                               40           45
232 Val Met Tyr Ala Glu Arg Arg Gly Val Arg Gln Asp Arg Ala Leu Ala
233 50                               55           60
235 Gln Glu Trp Leu Gly Lys Ala Cys Gln Asn Gly Tyr Gln Asp Ser Cys
236 65                               70           75           80
238 Asp Asn Asp Gln Arg Leu Lys Ala Gly Tyr
239                               85           90
242 <210> SEQ ID NO: 7
243 <211> LENGTH: 381
244 <212> TYPE: DNA
245 <213> ORGANISM: Neisseria gonorrhoeae
247 <400> SEQUENCE: 7
248 atgaaacaga cagtcaaatg gcttgccgcc gccctgattg ccttgggctt gaaccaagcg 60
249 gtgtgggcgg gtgacgtatc ggattttcgg gaaaacttgc aggcggcaga acagggaaat 120
250 gcagcagccc aattcaattt gggcgtgatg tatgaaaatg gacaaggagt tcgtcaagat 180
251 tatgtacagg cagtgcagtg gtatcgcaag gcttcagaac aaaggggatgc ccaagcccaa 240
252 tacaatttgg gcttgatgta ttacgatgga cgcggcgtgc gccaaagacct tgcgctcgct 300
253 caacaatggc ttggcaaggc ttgtcaaaac ggagacccaa acagctgcga caatgaccaa 360
254 cgcctgaagg cgggttatta a                               381
257 <210> SEQ ID NO: 8
258 <211> LENGTH: 126
259 <212> TYPE: PRT
260 <213> ORGANISM: Neisseria meningitidis
262 <400> SEQUENCE: 8
263 Met Lys Gln Thr Val Lys Trp Leu Ala Ala Ala Leu Ile Ala Leu Gly
264 1                               5           10           15

```

RAW SEQUENCE LISTING                      DATE: 10/12/2000  
 PATENT APPLICATION: US/09/303,518A        TIME: 15:29:08

Input Set : N:\jumbos\09303518  
 Output Set: N:\CRF3\10122000\I303518A.raw

```

266 Leu Asn Gln Ala Val Trp Ala Gly Asp Val Ser Asp Phe Arg Glu Asn
267           20           25           30
269 Leu Gln Ala Ala Glu Gln Gly Asn Ala Ala Gln Phe Asn Leu Gly
270           35           40           45
272 Val Met Tyr Glu Asn Gly Gln Gly Val Arg Gln Asp Tyr Val Gln Ala
273           50           55           60
275 Val Gln Trp Tyr Arg Lys Ala Ser Glu Gln Gly Asp Ala Gln Ala Gln
276           65           70           75           80
278 Tyr Asn Leu Gly Leu Met Tyr Tyr Asp Gly Arg Gly Val Arg Gln Asp
279           85           90           95
281 Leu Ala Leu Ala Gln Gln Trp Leu Gly Lys Ala Cys Gln Asn Gly Asp
282           100          105          110
284 Gln Asn Ser Cys Asp Asn Asp Gln Arg Leu Lys Ala Gly Tyr
285           115          120          125
288 <210> SEQ ID NO: 9
289 <211> LENGTH: 357
290 <212> TYPE: DNA
291 <213> ORGANISM: Neisseria meningitidis
293 <400> SEQUENCE: 9
294 ttcggcgaca tcggcggttt gaaggtcaat gcccccgta aatccgcagg cgtattggtc 60
295 gggcgcgctcg gcgctatcgg acttgaccgg aaatccctatc aggcgaggggt gcgcctcgat 120
296 ttggacggca agtatcagtt cagcagcgac gtttccgcgc aaatccctgac ttcsggactt 180
297 ttggcgagc agtacatcgg gctgcagcag ggcggcgaca cggaaaacct tgctgccggc 240
298 gacaccatct ccgtaaccag ttctgcaatg gttctggaaa accttatcgg caaatcatg 300
299 acgagttttg ccgagaaaaa tgccgacggc ggcaatgcgg aaaaagccgc cgaataa 357
302 <210> SEQ ID NO: 10
303 <211> LENGTH: 118
304 <212> TYPE: PRT
305 <213> ORGANISM: Neisseria meningitidis
307 <400> SEQUENCE: 10
308 Phe Gly Asp Ile Gly Gly Leu Lys Val Asn Ala Pro Val Lys Ser Ala
309 1 5 10 15
311 Gly Val Leu Val Gly Arg Val Gly Ala Ile Gly Leu Asp Pro Lys Ser
312 20 25 30
314 Tyr Gln Ala Arg Val Arg Leu Asp Leu Asp Gly Lys Tyr Gln Phe Ser
315 35 40 45
317 Ser Asp Val Ser Ala Gln Ile Leu Thr Ser Gly Leu Leu Gly Glu Gln
318 50 55 60
320 Tyr Ile Gly Leu Gln Gln Gly Gly Asp Thr Glu Asn Leu Ala Ala Gly
321 65 70 75 80
323 Asp Thr Ile Ser Val Thr Ser Ser Ala Met Val Leu Glu Asn Leu Ile
324 85 90 95
326 Gly Lys Phe Met Thr Ser Phe Ala Glu Lys Asn Ala Asp Gly Gly Asn
327 100 105 110
329 Ala Glu Lys Ala Ala Glu
330 115
333 <210> SEQ ID NO: 11
334 <211> LENGTH: 859
335 <212> TYPE: DNA

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09/30/88

6

<210> 23  
 <211> 903  
 <212> DNA  
 <213> Neisseria meningitidis

<400> 23  
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 gaacccgatt cgcgcgaaga cgtattgacc ctgttgccgc aagcgacga acaggaagta 120  
 tttgatgcgg atacgctddd aagattggaa aaagtcctcg atttttctga tttggaagtg 180  
 cgcgacgcga tgattacgcg cagccgtatg aacgttttaa aagaaaacga cagcatcgaa 240  
 cgcacacccg cctacgttat cgataccgcc cattcgcgct tccccgtcat cggatgaagac 300  
 aaagacgaag ttttgggtat tttgcacgcc aaagacctgc tcaaataatat gttcaacccc 360  
 gagcagttcc acctcaaate gatattgcgc cctgcgctct tcgtccccga aggcaaatcg 420  
 ctgaccgccc ttttaaaaga gttccgcgaa cagcgcaacc atatggcaat cgtcatcgac 480  
 gaatacggcg gcacgtcggg tttggttaact tttgaagaca tcatcgagca aatcgtcggc 540  
 gacatcgaag atgagtttga cgaagacgaa agcgcggaca acatccacgc cgtttccgcc 600  
 gaacgtctggc gcatccacgc ggetaccgaa atcgaagaca tcaacgcett tttcggcacg 660  
 gaatacagca gcgaagaagc cgacaccatc ggcggccttg gtcattcagg aattggacaa 720  
 cctgcccgtg cgcggcgaaa aagtccttat cggcgntttg canttcaadg tcgcccgcgc 780  
 ngacaaccgc cgcctgcata cgctgatggc gacccgcgtg aagtaagctc cgcgctttct 840  
 gtacagttta ggatgacggt acgggcgttt tctgtttcaa tccgccccat ccgccanaca 900  
 taa 903

see  
 item 10  
 on Enon  
 summary  
 sheet

FYI

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.



## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/303,518A

DATE: 10/12/2000

TIME: 15:29:09

Input Set : N:\jumbos\09303518

Output Set: N:\CRF3\10122000\I303518A.raw

L:59 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:822 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:831 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:834 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:931 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:23  
L:931 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23  
L:931 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23  
L:931 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23  
L:931 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23  
L:942 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:23  
L:942 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23  
L:942 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23  
L:942 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23  
M:340 Repeated in SeqNo=23  
L:943 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:23  
L:943 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23  
L:943 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23  
L:943 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23  
L:944 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:23  
L:944 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23  
L:944 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23  
L:944 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23  
L:945 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:23  
L:945 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23  
L:945 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23  
L:945 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23  
L:955 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:24  
L:955 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24  
L:955 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24  
L:955 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24  
L:955 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24  
L:997 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:24  
L:997 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24

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L:997 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24  
L:997 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24  
M:340 Repeated in SeqNo=24  
L:1000 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:24  
L:1000 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24  
L:1000 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24  
L:1000 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24  
L:1003 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:24  
L:1003 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24  
L:1003 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24  
L:1003 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24  
L:1009 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:24  
L:1009 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24  
L:1009 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24  
L:1009 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24  
L:1024 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:1224 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:30  
L:1224 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30  
L:1224 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30  
L:1224 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:30  
L:1224 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:30  
L:1230 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:30  
L:1230 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30  
L:1230 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30  
L:1230 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:30  
M:340 Repeated in SeqNo=30  
L:1441 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:1812 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:43  
L:1812 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:43  
L:1812 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:43  
M:340 Repeated in SeqNo=43  
L:1860 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:44  
M:340 Repeated in SeqNo=44  
L:1977 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45  
L:2270 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:50  
L:2437 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:53  
M:340 Repeated in SeqNo=53  
L:2473 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:54  
M:340 Repeated in SeqNo=54  
L:2590 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55  
L:2812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59  
L:2814 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59  
L:2815 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59  
L:2816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59  
L:2833 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:60  
M:340 Repeated in SeqNo=60  
L:2858 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:61  
M:340 Repeated in SeqNo=61  
L:2879 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:62

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M:340 Repeated in SeqNo=62  
L:3012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67  
L:3022 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:68  
M:340 Repeated in SeqNo=68  
L:3205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73  
L:3325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77  
L:3347 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:78  
M:340 Repeated in SeqNo=78  
L:3688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85  
L:3696 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85  
L:3718 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:86  
L:3769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87  
L:3824 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:88  
L:3922 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91  
L:4185 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:99  
M:340 Repeated in SeqNo=99  
L:4219 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:100  
M:340 Repeated in SeqNo=100  
L:4319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103  
L:4321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103  
L:4323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103  
L:4324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103  
L:4342 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:104  
M:340 Repeated in SeqNo=104  
L:4738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109  
L:5035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:113  
L:5040 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:113  
L:5053 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:113  
L:5054 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:113  
L:5075 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:114  
M:340 Repeated in SeqNo=114  
L:5312 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:117  
L:5388 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:118  
L:5442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:119  
L:5716 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:124  
L:5862 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:127  
M:340 Repeated in SeqNo=127  
L:5897 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:128  
M:340 Repeated in SeqNo=128  
L:5987 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129  
L:6193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:133  
L:6218 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:134  
M:340 Repeated in SeqNo=134  
L:6711 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:141  
M:340 Repeated in SeqNo=141  
L:6728 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:142  
M:340 Repeated in SeqNo=142  
L:6822 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:144  
L:6880 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:145

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L:6978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:147  
L:6982 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:147  
L:6983 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:147  
L:6996 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:148